

SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDES ENCODING A NOVEL HUMAN PHOSPHATASE, BMY_HPP13

<130> D0149 NP

<160> 40

<170> PatentIn version 3.2

<210> 1

<211> 989

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)..(763)

<400> 1

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                        1                      5

cag aca ttt caa gaa cta atc caa gag gca aaa ccc cgg gcc aca tgg      100
Gln Thr Phe Gln Glu Leu Ile Gln Glu Ala Lys Pro Arg Ala Thr Trp
10                      15                      20                      25

acg ctg aag ttg gat ggc aac ctt cag cta gac tgc ctg gct caa ggg      148
Thr Leu Lys Leu Asp Gly Asn Leu Gln Leu Asp Cys Leu Ala Gln Gly
                      30                      35                      40

tgg aag caa tac caa cag aga gca ttt ggc tgg ttc cgg tgt tcc tcc      196
Trp Lys Gln Tyr Gln Gln Arg Ala Phe Gly Trp Phe Arg Cys Ser Ser
                      45                      50                      55

tgc cag cga agt tgg gct tcc gcc caa gtg cag att ctg tgc cac acg      244
Cys Gln Arg Ser Trp Ala Ser Ala Gln Val Gln Ile Leu Cys His Thr
                      60                      65                      70

tac tgg gag cac tgg aca tcc cag ggt cag gtg cgt atg agg ctc ttt      292
Tyr Trp Glu His Trp Thr Ser Gln Gly Gln Val Arg Met Arg Leu Phe
75                      80                      85

ggc caa agg tgc cag aag tgc tcc tgg tcc caa tat gag atg cct gag      340
Gly Gln Arg Cys Gln Lys Cys Ser Trp Ser Gln Tyr Glu Met Pro Glu
90                      95                      100                      105

ttc tcc tcg gat agc acc atg agg att ctg agc aac ctg gtg cag cat      388
Phe Ser Ser Asp Ser Thr Met Arg Ile Leu Ser Asn Leu Val Gln His
110                      115                      120

ata ctg aag aaa tac tat gga aat ggc acg agg aag tct cca gaa atg      436
Ile Leu Lys Lys Tyr Tyr Gly Asn Gly Thr Arg Lys Ser Pro Glu Met

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125	130	135	
cca gta atc ctg gaa gtg tcc ctg gaa gga tcc cat gac aca gcc aat			484
Pro Val Ile Leu Glu Val Ser Leu Glu Gly Ser His Asp Thr Ala Asn			
140	145	150	
tgt gag gca tgc act ttg ggc atc tgt gga cag ggc tta aaa agc tgc			532
Cys Glu Ala Cys Thr Leu Gly Ile Cys Gly Gln Gly Leu Lys Ser Cys			
155	160	165	
atg aca aag ccg tcc aaa tcc cta ctc ccc cac cta aag act ggg aat			580
Met Thr Lys Pro Ser Lys Ser Leu Leu Pro His Leu Lys Thr Gly Asn			
170	175	180	185
tcc tca cct gga att ggt gct gtg tac ctc gca aac caa gcc aag aac			628
Ser Ser Pro Gly Ile Gly Ala Val Tyr Leu Ala Asn Gln Ala Lys Asn			
190	195	200	
cag tca gct gag gca aaa gag gct aag ggg agt ggg tat gag aaa tta			676
Gln Ser Ala Glu Ala Lys Glu Ala Lys Gly Ser Gly Tyr Glu Lys Leu			
205	210	215	
ggg ccc agt cga gac cca gat cca ctg aac atc tgt gtc ttt att ttg			724
Gly Pro Ser Arg Asp Pro Asp Pro Leu Asn Ile Cys Val Phe Ile Leu			
220	225	230	
ctg ctt gta ttt att gta gtc aaa tgc ttt aca tca gaa tgatgaaaat			773
Leu Leu Val Phe Ile Val Val Lys Cys Phe Thr Ser Glu			
235	240	245	
aggcttgcca ctttctctta ttttaattcc atggtagtca atgaactggc tgccacttta			833
atataactga aaattcattt tgagaccaag caggatcaag tttgtagaat aaacactggg			893
ttcctagcca tcctctgaaa acagtatgaa acatgaccaa gtacataatg gatttagtaa			953
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Gln	Glu	Ala	Lys	Pro	Arg	Ala	Thr	Trp	Thr	Leu	Lys	Leu	Asp	Gly	Asn
		20						25					30		

Leu	Gln	Leu	Asp	Cys	Leu	Ala	Gln	Gly	Trp	Lys	Gln	Tyr	Gln	Gln	Arg
		35					40					45			

Ala Phe Gly Trp Phe Arg Cys Ser Ser Cys Gln Arg Ser Trp Ala Ser
50 55 60

Ala Gln Val Gln Ile Leu Cys His Thr Tyr Trp Glu His Trp Thr Ser
65 70 75 80

Gln Gly Gln Val Arg Met Arg Leu Phe Gly Gln Arg Cys Gln Lys Cys
85 90 95

Ser Trp Ser Gln Tyr Glu Met Pro Glu Phe Ser Ser Asp Ser Thr Met
100 105 110

Arg Ile Leu Ser Asn Leu Val Gln His Ile Leu Lys Lys Tyr Tyr Gly
115 120 125

Asn Gly Thr Arg Lys Ser Pro Glu Met Pro Val Ile Leu Glu Val Ser
130 135 140

Leu Glu Gly Ser His Asp Thr Ala Asn Cys Glu Ala Cys Thr Leu Gly
145 150 155 160

Ile Cys Gly Gln Gly Leu Lys Ser Cys Met Thr Lys Pro Ser Lys Ser
165 170 175

Leu Leu Pro His Leu Lys Thr Gly Asn Ser Ser Pro Gly Ile Gly Ala
180 185 190

Val Tyr Leu Ala Asn Gln Ala Lys Asn Gln Ser Ala Glu Ala Lys Glu
195 200 205

Ala Lys Gly Ser Gly Tyr Glu Lys Leu Gly Pro Ser Arg Asp Pro Asp
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Pro Leu Asn Ile Cys Val Phe Ile Leu Leu Leu Val Phe Ile Val Val
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Lys Cys Phe Thr Ser Glu
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<210> 3

<211> 624

<212> DNA

<213> Homo sapiens

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aac tgg atc ttc aac cca ggt tcc ggt gtt cct cct gcc agc gaa gtt	96
Asn Trp Ile Phe Asn Pro Gly Ser Gly Val Pro Pro Ala Ser Glu Val	
20 25 30	
ggg ctt ccg ccc aag tgc aga ttc tgt gcc aca cgt act ggg agc act	144
Gly Leu Pro Pro Lys Cys Arg Phe Cys Ala Thr Arg Thr Gly Ser Thr	
35 40 45	
gga cat ccc agg gtc agg tgc cag aag tgc tcc tgg tcc caa tat gag	192
Gly His Pro Arg Val Arg Cys Gln Lys Cys Ser Trp Ser Gln Tyr Glu	
50 55 60	
atg cct gag ttc tcc tcg gat agc acc atg agg att ctg agc aac ctg	240
Met Pro Glu Phe Ser Ser Asp Ser Thr Met Arg Ile Leu Ser Asn Leu	
65 70 75 80	
gtg cag cat ata ctg aag aaa tac tat gga aat ggc acg agg aag tct	288
Val Gln His Ile Leu Lys Lys Tyr Tyr Gly Asn Gly Thr Arg Lys Ser	
85 90 95	
cca gaa atg cca gta atc ctg gaa gtg tcc ctg gaa gga tcc cat gac	336
Pro Glu Met Pro Val Ile Leu Glu Val Ser Leu Glu Gly Ser His Asp	
100 105 110	
aca gcc aat tgt gag gca tgc act ttg ggc atc tgt gga cag ggc tta	384
Thr Ala Asn Cys Glu Ala Cys Thr Leu Gly Ile Cys Gly Gln Gly Leu	
115 120 125	
aaa agc tgc atg aca aag ccg tcc aaa tcc cta ctc ccc cac cta aag	432
Lys Ser Cys Met Thr Lys Pro Ser Lys Ser Leu Leu Pro His Leu Lys	
130 135 140	
act ggg aat tcc tca cct gga att ggt gct gtg tac ctc gca aac caa	480
Thr Gly Asn Ser Ser Pro Gly Ile Gly Ala Val Tyr Leu Ala Asn Gln	
145 150 155 160	
gcc aag aac cag tca gct gag gca aaa gag gct aag ggg agt ggg tat	528
Ala Lys Asn Gln Ser Ala Glu Ala Lys Glu Ala Lys Gly Ser Gly Tyr	
165 170 175	
gag aaa tta ggg ccc agt cga gac cca gat cca ctg aac atc tgt gtc	576
Glu Lys Leu Gly Pro Ser Arg Asp Pro Asp Pro Leu Asn Ile Cys Val	
180 185 190	
ttt att ttg ctg ctt gta ttt att gta gtc aaa tgc ttt aca tca gaa	624
Phe Ile Leu Leu Leu Val Phe Ile Val Val Lys Cys Phe Thr Ser Glu	

195

200

205

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 <213> Homo sapiens

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Met Arg Val Ile Glu Gly Lys Gly Phe Ala Gln Gly Leu Pro Asp Val
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Asn Trp Ile Phe Asn Pro Gly Ser Gly Val Pro Pro Ala Ser Glu Val
 20 25 30

Gly Leu Pro Pro Lys Cys Arg Phe Cys Ala Thr Arg Thr Gly Ser Thr
 35 40 45

Gly His Pro Arg Val Arg Cys Gln Lys Cys Ser Trp Ser Gln Tyr Glu
 50 55 60

Met Pro Glu Phe Ser Ser Asp Ser Thr Met Arg Ile Leu Ser Asn Leu
 65 70 75 80

Val Gln His Ile Leu Lys Lys Tyr Tyr Gly Asn Gly Thr Arg Lys Ser
 85 90 95

Pro Glu Met Pro Val Ile Leu Glu Val Ser Leu Glu Gly Ser His Asp
 100 105 110

Thr Ala Asn Cys Glu Ala Cys Thr Leu Gly Ile Cys Gly Gln Gly Leu
 115 120 125

Lys Ser Cys Met Thr Lys Pro Ser Lys Ser Leu Leu Pro His Leu Lys
 130 135 140

Thr Gly Asn Ser Ser Pro Gly Ile Gly Ala Val Tyr Leu Ala Asn Gln
 145 150 155 160

Ala Lys Asn Gln Ser Ala Glu Ala Lys Glu Ala Lys Gly Ser Gly Tyr
 165 170 175

Glu Lys Leu Gly Pro Ser Arg Asp Pro Asp Pro Leu Asn Ile Cys Val
 180 185 190

Phe Ile Leu Leu Leu Val Phe Ile Val Val Lys Cys Phe Thr Ser Glu
195 200 205

<210> 5
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Asp Tyr Ile Asn Ala Ser Asn
1 5

<210> 6
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<222> (2)..(3)
<223> wherein "X" equals any naturally occuring amino acid.

<400> 6

Cys Xaa Xaa Tyr Trp Pro
1 5

<210> 7
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<220>
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<222> (5)..(8)
<223> wherein "X" equals any naturally occuring amino acid.

<400> 7

Ile Val Val Met Xaa Xaa Xaa Xaa Glu
1 5

<210> 8
<211> 8
<212> PRT
<213> HOMO SAPIENS

<400> 8

Asp Asn Tyr Ile Asn Ala Ser Asn
1 5

<210> 9
<211> 6
<212> PRT
<213> HOMO SAPIENS

<220>
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<222> (2) .. (3)
<223> wherein "X" equals any naturally occurring amino acid.

<400> 9

Cys Xaa Xaa Tyr Trp Pro
1 5

<210> 10
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<213> HOMO SAPIENS

<220>
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<223> wherein "X" equals any naturally occurring amino acid.

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Ile Val Val Met Xaa Xaa Xaa Xaa Glu
1 5

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<212> PRT
<213> HOMO SAPIENS

<400> 11

Met Glu Val Pro Gln Pro Glu Pro Ala Pro Gly Ser Ala Leu Ser Pro
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Ala Gly Val Cys Gly Gly Ala Gln Arg Pro Gly His Leu Pro Gly Leu
20 25 30

Leu Leu Gly Ser His Gly Leu Leu Gly Ser Pro Val Arg Ala Ala Ala
35 40 45

Ser Ser Pro Val Thr Thr Leu Thr Gln Thr Met His Asp Leu Ala Gly
 50 55 60

Leu Gly Ser Arg Ser Arg Leu Thr His Leu Ser Leu Ser Arg Arg Ala
 65 70 75 80

Ser Glu Ser Ser Leu Ser Ser Glu Ser Ser Glu Ser Ser Asp Ala Gly
 85 90 95

Leu Cys Met Asp Ser Pro Ser Pro Met Asp Pro His Met Ala Glu Gln
 100 105 110

Thr Phe Glu Gln Ala Ile Gln Ala Ala Ser Arg Ile Ile Arg Asn Glu
 115 120 125

Gln Phe Ala Ile Arg Arg Phe Gln Ser Met Pro Val Arg Leu Leu Gly
 130 135 140

His Ser Pro Val Leu Arg Asn Ile Thr Asn Ser Gln Ala Pro Asp Gly
 145 150 155 160

Arg Arg Lys Ser Glu Ala Gly Ser Gly Ala Ala Ser Ser Ser Gly Glu
 165 170 175

Asp Lys Glu Asn Asp Gly Phe Val Phe Lys Met Pro Trp Lys Pro Thr
 180 185 190

His Pro Ser Ser Thr His Ala Leu Ala Glu Trp Ala Ser Arg Arg Glu
 195 200 205

Ala Phe Ala Gln Arg Pro Ser Ser Ala Pro Asp Leu Met Cys Leu Ser
 210 215 220

Pro Asp Arg Lys Met Glu Val Glu Glu Leu Ser Pro Leu Ala Leu Gly
 225 230 235 240

Arg Phe Ser Leu Thr Pro Ala Glu Gly Asp Thr Glu Glu Asp Asp Gly
 245 250 255

Phe Val Asp Ile Leu Glu Ser Asp Leu Lys Asp Asp Asp Ala Val Pro
 260 265 270

Pro Gly Met Glu Ser Leu Ile Ser Ala Pro Leu Val Lys Thr Leu Glu

275		280		285
Lys Glu Glu Glu Lys Asp Leu Val Met Tyr Ser Lys Cys Gln Arg Leu	290	295	300	
Phe Arg Ser Pro Ser Met Pro Cys Ser Val Ile Arg Pro Ile Leu Lys	305	310	315	320
Arg Leu Glu Arg Pro Gln Asp Arg Asp Thr Pro Val Gln Asn Lys Arg	325	330	335	
Arg Arg Ser Val Thr Pro Pro Glu Glu Gln Gln Glu Ala Glu Glu Pro	340	345	350	
Lys Ala Arg Val Leu Arg Ser Lys Ser Leu Cys His Asp Glu Ile Glu	355	360	365	
Asn Leu Leu Asp Ser Asp His Arg Glu Leu Ile Gly Asp Tyr Ser Lys	370	375	380	
Ala Phe Leu Leu Gln Thr Val Asp Gly Lys His Gln Asp Leu Lys Tyr	385	390	395	400
Ile Ser Pro Glu Thr Met Val Ala Leu Leu Thr Gly Lys Phe Ser Asn	405	410	415	
Ile Val Asp Lys Phe Val Ile Val Asp Cys Arg Tyr Pro Tyr Glu Tyr	420	425	430	
Glu Gly Gly His Ile Lys Thr Ala Val Asn Leu Pro Leu Glu Arg Asp	435	440	445	
Ala Glu Ser Phe Leu Leu Lys Ser Pro Ile Ala Pro Cys Ser Leu Asp	450	455	460	
Lys Arg Val Ile Leu Ile Phe His Cys Glu Phe Ser Ser Glu Arg Gly	465	470	475	480
Pro Arg Met Cys Arg Phe Ile Arg Glu Arg Asp Arg Ala Val Asn Asp	485	490	495	
Tyr Pro Ser Leu Tyr Tyr Pro Glu Met Tyr Ile Leu Lys Gly Gly Tyr	500	505	510	

Lys Glu Phe Phe Pro Gln His Pro Asn Phe Cys Glu Pro Gln Asp Tyr
515 520 525

Arg Pro Met Asn His Glu Ala Phe Lys Asp Glu Leu Lys Thr Phe Arg
530 535 540

Leu Lys Thr Arg Ser Trp Ala Gly Glu Arg Ser Arg Arg Glu Leu Cys
545 550 555 560

Ser Arg Leu Gln Asp Gln
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gccagagggtgc cgtaaaggctc attttctgac gtttgaaaaa caacgccaca attgagaaat 120
cgacgacggt cggtcgagat ggtatgatgc gtaataaact atcccccaag attcgagggt 180
cgacgaactgc ggaggagagt gatgcacgcg ccaatgtatc cgtaggatta tg 232

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<210> 14
<211> 18
<212> DNA
<213> Homo sapiens

<400> 14
cttcgctggc aggaggaa 18

<210> 15
<211> 24
<212> DNA
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<400> 15

ccggaaccag ccaaatgctc tctg

24

<210> 16
<211> 525
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<213> HOMO SAPIENS

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Glu	Asn	Leu	Leu	Leu	Thr	Arg	Gly	Val	Asp	Gly	Ser	Phe	Leu	Ala	Arg	
		20						25					30			
Pro	Ser	Lys	Ser	Asn	Pro	Gly	Asp	Leu	Thr	Leu	Ser	Val	Arg	Arg	Asn	
		35					40					45				
Gly	Ala	Val	Thr	His	Ile	Lys	Ile	Gln	Asn	Thr	Gly	Asp	Tyr	Tyr	Asp	
	50					55					60					
Leu	Tyr	Gly	Gly	Glu	Lys	Phe	Ala	Thr	Leu	Ala	Glu	Leu	Val	Gln	Tyr	
65					70					75					80	
Tyr	Met	Glu	His	His	Gly	Gln	Leu	Lys	Glu	Lys	Asn	Gly	Asp	Val	Ile	
				85					90					95		
Glu	Leu	Lys	Tyr	Pro	Leu	Asn	Cys	Ala	Asp	Pro	Thr	Ser	Glu	Arg	Trp	
			100					105						110		
Phe	His	Gly	His	Leu	Ser	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Leu	Thr	Glu	
		115					120						125			
Lys	Gly	Lys	His	Gly	Ser	Phe	Leu	Val	Arg	Glu	Ser	Gln	Ser	His	Pro	
	130					135						140				
Gly	Asp	Phe	Val	Leu	Ser	Val	Arg	Thr	Gly	Asp	Asp	Lys	Gly	Glu	Ser	
145					150					155					160	
Asn	Asp	Gly	Lys	Ser	Lys	Val	Thr	His	Val	Met	Ile	Arg	Cys	Gln	Glu	
			165						170					175		
Leu	Lys	Tyr	Asp	Val	Gly	Gly	Gly	Glu	Arg	Phe	Asp	Ser	Leu	Thr	Asp	
			180					185					190			

Leu Val Glu His Tyr Lys Lys Asn Pro Met Val Glu Thr Leu Gly Thr
 195 200 205

Val Leu Gln Leu Lys Gln Pro Leu Asn Thr Thr Arg Ile Asn Ala Ala
 210 215 220

Glu Ile Glu Ser Arg Val Arg Glu Leu Ser Lys Leu Ala Glu Thr Thr
 225 230 235 240

Asp Lys Val Lys Gln Gly Phe Trp Glu Glu Phe Glu Thr Leu Gln Gln
 245 250 255

Gln Glu Cys Lys Leu Leu Tyr Ser Arg Lys Glu Gly Gln Arg Gln Glu
 260 265 270

Asn Lys Asn Lys Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Thr
 275 280 285

Arg Val Val Leu His Asp Gly Asp Pro Asn Glu Pro Val Ser Asp Tyr
 290 295 300

Ile Asn Ala Asn Ile Ile Met Pro Glu Phe Glu Thr Lys Cys Asn Asn
 305 310 315 320

Ser Lys Pro Lys Lys Ser Tyr Ile Ala Thr Gln Gly Cys Leu Gln Asn
 325 330 335

Thr Val Asn Asp Phe Trp Arg Met Val Phe Gln Glu Asn Ser Arg Val
 340 345 350

Ile Val Met Thr Thr Lys Glu Val Glu Arg Gly Lys Ser Lys Cys Val
 355 360 365

Lys Tyr Trp Pro Asp Glu Tyr Ala Leu Lys Glu Tyr Gly Val Met Arg
 370 375 380

Val Arg Asn Val Lys Glu Ser Ala Ala His Asp Tyr Thr Leu Arg Glu
 385 390 395 400

Leu Lys Leu Ser Lys Val Gly Gln Gly Asn Thr Glu Arg Thr Val Trp
 405 410 415

Gln Tyr His Phe Arg Thr Trp Pro Asp His Gly Val Pro Ser Asp Pro
 420 425 430

Gly Gly Val Leu Asp Phe Leu Glu Glu Val His His Lys Gln Glu Ser
 435 440 445

Ile Met Asp Ala Gly Pro Val Val Val His Cys Ser Ala Gly Ile Gly
 450 455 460

Arg Thr Gly Thr Phe Ile Val Ile Asp Ile Leu Ile Asp Ile Ile Arg
 465 470 475 480

Glu Lys Gly Val Asp Cys Asp Ile Asp Val Pro Lys Thr Ile Gln Met
 485 490 495

Val Arg Ser Gln Arg Ser Gly Met Val Gln Thr Glu Ala Gln Tyr Arg
 500 505 510

Ser Ile Tyr Met Ala Val Gln His Tyr Ile Glu Thr Leu
 515 520 525

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Lys Lys Tyr Tyr Gly Asn Gly Thr Arg Lys Ser Pro Glu Met
 1 5 10

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Ala Asn Gln Ala Lys Asn Gln Ser Ala Glu Ala Lys Glu Ala
 1 5 10

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Pro Arg Ala Thr Trp Thr Leu Lys Leu Asp Gly Asn Leu
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Phe Ser Ser Asp Ser Thr Met Arg Ile Leu Ser Asn Leu
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Tyr Tyr Gly Asn Gly Thr Arg Lys Ser Pro Glu Met Pro
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Trp Thr Trp Glu Gln Thr Phe Gln Glu Leu Ile Gln Glu Ala
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Gln Ile Leu Cys His Thr Tyr Trp Glu His Trp Thr Ser Gln
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Gln Lys Cys Ser Trp Ser Gln Tyr Glu Met Pro Glu Phe Ser
1 5 10

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Lys Glu Ala Lys Gly Ser Gly Tyr Glu Lys Leu Gly Pro Ser
 1 5 10

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 1 5 10 15

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Gly Ile Cys Gly Gln Gly Leu Lys Ser Cys Met Thr Lys Pro Ser Lys
 1 5 10 15

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 atttaggtga cactatag 18

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 agctgactgg ttcttggtt 20

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Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 34
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 tctcccgga tcttgaggtc acatgcgtgg tggaggacgt aagccacgaa gacctgagg 180
 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
 aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
 ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccatcg 360
 agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
 catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct 480

atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga	540
ccacgcctcc cgtgctggac tccgacggct ctttcttctt ctacagcaag ctcaccgtgg	600
acaagagcag gtggcagcag gggaaacgtct tctcatgctc cgtgatgcat gaggctctgc	660
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gcagcagtcg accccactcc ccttagcctc ttttgcc	37

<210> 39
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<400> 39

Pro	Leu	Asn	Ile	Cys	Val	Phe	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Val
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Lys Cys Phe

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<400> 40

Glu Met Glu Lys Glu Phe Glu Gln Ile Asp Lys Ser Gly Ser Trp Ala
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Ala Ile Tyr Gln Asp Ile Arg His Glu Ala Ser Asp Phe Pro Cys Arg
20 25 30

Val Ala Lys Leu Pro Lys Asn Lys Asn Arg Asn Arg Tyr Arg Asp Val
35 40 45

Ser Pro Phe Asp His Ser Arg Ile Lys Leu His Gln Glu Asp Asn Asp
50 55 60

Tyr Ile Asn Ala Ser Leu Ile Lys Met Glu Glu Ala Gln Arg Ser Tyr
65 70 75 80

Ile Leu Thr Gln Gly Pro Leu Pro Asn Thr Cys Gly His Phe Trp Glu
85 90 95

Met Val Trp Glu Gln Lys Ser Arg Gly Val Val Met Leu Asn Arg Val
100 105 110

Met Glu Lys Gly Ser Leu Lys Cys Ala Gln Tyr Trp Pro Gln Lys Glu
115 120 125

Glu Lys Glu Met Ile Phe Glu Asp Thr Asn Leu Lys Leu Thr Leu Ile
130 135 140

Ser Glu Asp Ile Lys Ser Tyr Tyr Thr Val Arg Gln Leu Glu Leu Glu
145 150 155 160

Asn Leu Thr Thr Gln Glu Thr Arg Glu Ile Leu His Phe His Tyr Thr
165 170 175

Thr Trp Pro Asp Phe Gly Val Pro Glu Ser Pro Ala Ser Phe Leu Asn
180 185 190

Phe Leu Phe Lys Val Arg Glu Ser Gly Ser Leu Ser Pro Glu His Gly
195 200 205

Pro Val Val Val His Ser Ser Ala Gly Ile Gly Arg Ser Gly Thr Phe
210 215 220

Cys Leu Ala Asp Thr Cys Leu Leu Leu Met Asp Lys Arg Lys Asp Pro
225 230 235 240

Ser Ser Val Asp Ile Lys Lys Val Leu Leu Glu Met Arg Lys Phe Arg
245 250 255

Met Gly Leu Ile Gln Thr Ala Asp Gln Leu Arg Phe Ser Tyr Leu Ala
260 265 270

Val Ile Glu Gly Ala Lys Phe Ile Met Gly Asp Ser Ser Val Gln Asp
275 280 285

Gln Trp Lys Glu Leu Ser His Glu Asp
290 295